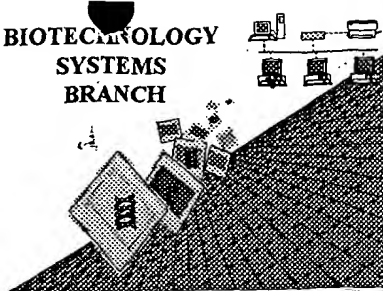


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



BC

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/857,525
Source: PCT/09
Date Processed by STIC: 10/30/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

ERROR DETECTED**SUGGESTED CORRECTION**SERIAL NUMBER: 09/857,525

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,525

DATE: 10/30/2001

TIME: 12:58:09

Input Set : A:\BB1316 PCT Seq List.txt

Output Set: N:\CRF3\10302001\I857525.raw

Does Not Comply
Corrected Diskette Needed

pp 1-2

3 <110> APPLICANT: E. I. du Pont de Nemours and Company
 5 <120> TITLE OF INVENTION: Plant Catabolite Repression Genes
 7 <130> FILE REFERENCE: BB1316
 9 <140> CURRENT APPLICATION NUMBER: US/09/857,525
 10 <141> CURRENT FILING DATE: 2001-09-10
 12 <150> PRIOR APPLICATION NUMBER: 60/112,564
 13 <151> PRIOR FILING DATE: 1998-12-16
 15 <160> NUMBER OF SEQ ID NOS: 22
 17 <170> SOFTWARE: Microsoft Office 97

ERRORED SEQUENCES

E--> 880 <210> *16 insert*
 881 <211> LENGTH: ~~16~~ 59
 882 <212> TYPE: PRT
 883 <213> ORGANISM: Zea mays
 885 <220> FEATURE:
 886 <221> NAME/KEY: UNSURE
 887 <222> LOCATION: (50)
 OK-> 889 <400> SEQUENCE: 16
 890 Val Ser Glu Tyr Leu Asn Leu His Thr Cys Tyr Asp Leu Leu Pro Asp
 891 1 5 10 15
 893 Ser Gly Lys Val Ile Ala Leu Asp Ile Asn Leu Pro Val Lys Gln Ser
 894 20 25 30
 896 Phe His Ile Leu His Glu Gln Gly Ile Pro Val Ala Pro Leu Trp Asp
 897 35 40 45
 W--> 899 Ser Xaa Lys Gly Gln Phe Gly Gly Pro Leu Ser → see item 9 on
 E--> 900 50 55 Ena summary
 999 <210> SEQ ID NO: 21
 1000 <211> LENGTH: 514
 1001 <212> TYPE: DNA
 1002 <213> ORGANISM: Triticum aestivum
 1004 <400> SEQUENCE: 21
 1005 cttagatcaa atcagcatct agtgcattgcc accccttatg aatccttgag gggatttgcc 60
 1006 atgaaaatac tcgaaactgg catttctaca gtcccaatca tctattcatc gtcattcagat 120
 1007 ggatcgtttc cgcagctgtt gcatcttgca tccctttcag gaattttgaa atgtatctgt 180
 1008 agatacttca agaactccac tggtagtttg ccgattctaa accaaccagt atgctcaatt 240
 1009 ccgctggggg acctgggggt ccaaaaaatg ggtgaaccaa atggcatcca ttgggtatgt 300
 E--> 1010 tgccggccta atacatctct taactctgcc cttaacttgt tgggtcaagc tgggagtat 360 → item 9
 E--> 1011 tcaataccca ttgggtgggat gataacgac cccttatttg acacataccc aagaagtgc 420 → item 9
 E--> 1012 atcacatct ngcgaaagha aggctacacc ataccgccta gattagatga catcaacaag 480 → item 9
 1013 gctgcaactc gggcaagacc gaatcacttt gggg 514
 1015 <210> SEQ ID NO: 22
 1016 <211> LENGTH: 77
 1017 <212> TYPE: PRT
 1018 <213> ORGANISM: Triticum aestivum

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,525

DATE: 10/30/2001

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Input Set : A:\BB1316 PCT Seq List.txt

Output Set: N:\CRF3\10302001\I857525.raw

1020 <400> SEQUENCE: 22

1021 Leu Val His Ala Thr Pro Tyr Glu Ser Leu Arg Gly Ile Ala Met Lys

1022 1 5 10 15

1024 Ile Leu Glu Thr Gly Ile Ser Thr Val Pro Ile Ile Tyr Ser Ser Ser

1025 20 25 30

1027 Ser Asp Gly Ser Phe Pro Gln Leu Leu His Leu Ala Ser Leu Ser Gly

1028 35 40 45

1030 Ile Leu Lys Cys Ile Cys Arg Tyr Phe Lys Asn Ser Thr Gly Ser Leu

1031 50 55 60

1033 Pro Ile Leu Asn Gln Pro Val Cys Ser Ile Pro Leu Gly

1034 65 70 75

--> 1036 18

delete

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/857,525

DATE: 10/30/2001

TIME: 12:58:10

Input Set : A:\BB1316 PCT Seq List.txt

Output Set: N:\CRF3\10302001\I857525.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
 L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:878 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
 L:878 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
 L:880 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:889 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:16
 L:899 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16
 L:899 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
 L:900 M:252 E: No. of Seq. differs, <211>LENGTH:Input:16 Found:59 SEQ:0
 L:924 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
 L:924 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:928 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
 L:928 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:944 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18
 L:944 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
 L:1010 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:21
 M:340 Repeated in SeqNo=21
 L:1036 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22